AMENDMENTS

Applicants respectfully request that the following amendments be entered.

IN THE SPECIFICATION

On page 11, line 12, please change "(SEQ ID NO:5)" to --(SEQ ID NO:4)--.

On page 11, line 30, please change "Also depicted is" to --SEQ ID NO:4 depicts--.

On page 11, line 31, please change "for GDNF" to --for rat GDNF--.

On page 11, line 31, please change "The nucleic acid" to --In Figure 13, the nucleic acid--.

On page 13, line 20, please change "Also depicted is" to --SEQ ID NO:6 depicts--.

On page 13, line 22, please change "The amino acid" to --In Figure 19, the amino acid--.

A revised Sequence Listing was submitted on January 16, 1998. The revision provides a separate listing (i.e., SEQ ID NO:26) for the amino acid sequence depicted in SEQ ID NO:25. The pre-pro glial cell line-derived neurotrophic factor polypeptide sequence is depicted by amino acid residues 10-220. Please amend the specification by inserting the revised Sequence Listing.

To further clarify the sequence information for SEQ ID NO:26 and SEQ ID NO:25 as discussed in the first response, Applicants request that the following amendments be entered, no new matter or issues are presented with these amendments:

On page 67, line 16, after "pre-proGDNF" please insert --(i.e., between the T and CA forming the codon for the serine residue at position 51)--

On page 67, line 23, after "NO:8)" please insert --. SEQ ID NO:25 and SEQ ID NO:26 present nucleotide and amino acid sequences, respectively, for a composite pre-pro sequence as depicted in Figures 22 and 19 as well as SEQ ID NOS:8 and 5. A pre-pro form of human glial cell line-derived neurotrophic factor polypeptide is set forth in SEQ ID NO:26 amino acid residues 10 through 220.--

On page 20, line 22 after "reference.", please insert:

> --In particular, Dayhoff describes that "[i]n practice, two related proteins may be aligned with the insertion of an average of 3 or 4 gaps in a length of 100 residues. About 20% of the aligned amino acids are identical. Under these conditions, the statistical conclusion of common ancestry can be drawn with great confidence. Common ancestry may exist even though it cannot be proved from the comparison of two sequences. The use of additional evidence, such as the correspondence of the active sites, the comparisons of many related sequences with one new one, and the nature of the three-dimensional structures, will eventually permit the inference of relationships of even more remotely related structures."--

IN THE CLAIMS:

88. **(Amended)** A purified and [recombinant or] isolated nucleic acid sequence encoding a glial cell line-derived neurotrophic factor polypeptide comprising an amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:6 and further comprising an amino-terminal methionine residue.